

OM nucleic - nucleic search, using sw model

Run on: July 7, 2004, 17:46:47 ; Search time 1892.13 Seconds
(without alignments)
16080.756 Million cell updates/sec

Title: US-10-018-786-7
Perfect score: 702
Sequence: 1 atgcgtctttgctgaggtc.....cagtcgaggtctgtgtga 702

Scoring table: IDENTITY_NUC
Gapex 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:
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3: gb_in:
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7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_uni:
14: gb_vi:
15: em_ba:
16: em_fun:
17: em_hum:
18: em_in:
19: em_mu:
20: em_om:
21: em_or:
22: em_ov:
23: em_pat:
24: em_ph:
25: em_pl:
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27: em_sts:

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31: em_htg_inv:
32: em_htg_other:
33: em_htg_mus:
34: em_htg_pln:
35: em_htg_rnd:
36: em_htg_mam:
37: em_htg_vrt:
38: em_sy:
39: em_htgo_hum:
40: em_htgo_mus:
41: em_htgo_other:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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	3	479.6	68.3	16929	1	XCU3548		U33548	Xanthomonas
	4	474.8	67.6	13551	1	AE011666		AE011666	Xanthomon
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c	8	460.4	65.6	19304	1	AB045311		AB045311	Xanthomon
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	16	69.6	9.9	138390	14	AY261359		AY261359	Bovine he
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	33	64.4	9.2	239130	2	AC079420		AC079420	Mus muscu

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ALIGNMENTS

RESULT 1
AX061806
LOCUS AX061806 702 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 7 from Patent WO0078967.
ACCESSION AX061806
VERSION AX061806.1 GI:12539886
KEYWORDS
SOURCE Xanthomonas campestris
ORGANISM Xanthomonas campestris
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
REFERENCE
1 Pierrard, J., Simon, J.L. and Chevallereau, P.
A virulent xanthomonas-campestris strains producing xanthan
Patent: WO 0078967-A 7 28-DEC-2000;
RHODIA CHIMIE (FR)
TITLES
JOURNAL
FEATURES
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Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Xanthomonas campestris pv. campestris str. ATCC 33913, section 130
of 460 of the complete genome.
ACCESSION AE012222 AE008922
VERSION AE012222.1 GI:21112273
KEYWORDS
SOURCE Xanthomonas campestris pv. campestris str. ATCC 33913
ORGANISM Xanthomonas campestris pv. campestris str. ATCC 33913
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
REFERENCE
1 (bases 1 to 11629)
AUTHORS da Silva, A.C.R., Ferro, J.A., Reinach, F.C., Farah, C.S., Furlan, L.R.,
Quaggio, R.B., Monteiro-Vitorello, C.B., Van Sluys, M.A., Almeida
Jr., N.F., Alves, L.M.C., do Amaral, A.M., Bertolini, M.C.,
Camargo, L.E.A., Camarotte, G., Cannavan, F., Cardozo, J.,
Chamargo, F., Clepine, L.P., Cicalelli, R.M.B., Coutinho, L.L.,
Cursino-Santos, J.R., El-Dorri, H., Faria, J.B., Ferreira, A.J.S.,
Ferreira, R.C.C., Ferro, M.I.T., Formighieri, E.F., Franco, M.C.,
Greggio, C.C., Gruber, A.K., Katsuyama, A.M., Kishi, L.T., Leite

Jr., R.P., Lemos, E.G.M., Lemos, M.V.F., Locali, E.C., Machado, M.A., Madalena, A.M.B.N., Martinez-Rossi, N.M., Martins, E.C., Meidanis, J., Menck, C.F.M., Miyaki, C.Y., Moon, D.H., Moreira, L.M., Novo, M.T.M., Okura, V.K., Oliveira, M.C., Oliveira, V.R., Pereira Jr., H.A., Rossi, A., Sena, J.A.D., Silva, C., de Souza, R.F., Spinola, L.A.F., Takita, M.A., Tamura, R.E., Teixeira, E.C., Tezza, R.I.D., Trindade dos Santos, M., Truffi, D., Tsai, S.M., White, F.F., Setubal, J.C. and Kitajima, J.P.

TITLE
Comparison of the genomes of two Xanthomonas pathogens with differing host specificities

JOURNAL
Nature 417 (6897), 459-463 (2002)

REFERENCE
2022145

PUBMED
1204217

AUTHORS
2 (bases 1 to 11629)

da Silva, A.C.R., Ferro, J.A., Reinach, F.C., Farah, C.S., Furlan, L.R., Quaggio, R.B., Monteiro-Vitorello, C.B., Van Sluys, M.A., Almeida Jr., N.F., Alves, L.M.C., do Amaral, A.M., Bertolini, M.C., Camargo, L.E.A., Camarotte, G., Cannavan, F., Cardozo, J., Chambergo, F., Capina, L.P., Cicarelli, R.M.B., Coutinho, L.L., Cursino-Santos, J.R., El-Dorri, H., Faria, J.B., Ferreira, A.J.S., Ferreira, R.C.C., Gruber, A., Katsuyama, A.M., Kishi, L.T., Leite Jr., R.P., Lemos, E.G.M., Lemos, M.V.F., Locali, E.C., Machado, M.A., Madeira, A.M.B.N., Martinez-Rossi, N.M., Martins, E.C., Meidanis, J., Menck, C.F.M., Miyaki, C.Y., Moon, D.H., Moreira, L.M., Novo, M.T.M., Okura, V.K., Oliveira, M.C., Oliveira, V.R., Pereira Jr., H.A., Rossi, A., Sena, J.A.D., Silva, C., de Souza, R.F., Spinola, L.A.F., Takita, M.A., Tamura, R.E., Teixeira, E.C., Tezza, R.I.D., Trindade dos Santos, M., Truffi, D., Tsai, S.M., White, F.F., Setubal, J.C. and Kitajima, J.P.

TITLE
Direct Submission

JOURNAL
Submitted (28-NOV-2001) Departamento de Bioquímica, Universidade de São Paulo, Av. Prof. Lineu Prestes 748, São Paulo, SP 05508-900, Brazil

FEATURES
source

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Job time : 1897.13 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2004, 17:42:57 ; Search time 205.168 Seconds
(without alignments)
14535.578 Million cell updates/sec

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Perfect score: 702
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 337863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0s
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	702	100.0	702	5 ABL57895	ABL57895 Partial h
2	74	10.5	113193	7 AAD54645	Aad54645 Streptomy
3	67.2	9.6	6297	7 AAD54236	Aad54236 Streptomy
4	67.2	9.6	50543	7 AAD54230	Aad54230 Streptomy
5	67	9.5	114955	2 AAX53491	Aax53491 Human ade
6	65.4	9.3	2247	7 AAL61177	Aal61177 Actinosyn
7	65.4	9.3	82746	7 AAL61224	Aal61224 Actinosyn

8	65	9.3	11238	7	AAD55817
9	65	9.3	60156	7	AAD55810
10	64.6	9.2	114955	2	AA533491
11	64.2	9.1	8438	2	AAQ73500
12	63.6	9.1	53789	2	AAV21187
13	62.8	8.9	4341	7	ABT32151
14	62.8	8.9	32539	7	ABT32129
15	62.4	8.9	3957	5	AAA09686
16	62.4	8.9	154746	6	AAD25519
17	62.4	8.9	154746	6	AAD25519
18	62.2	8.9	1771	2	AA762138
19	62.2	8.9	1771	2	AAV47558
20	62.2	8.9	1771	2	AAZ55621
21	62.2	8.9	1771	6	AAAD40285
22	62.2	8.9	1771	6	AAAS96022
23	62.2	8.9	1771	6	ABK81733
24	62.2	8.9	1771	6	AAF88524
25	62.2	8.9	1771	8	ADB78770
26	61.8	8.8	9222	7	AA161171
27	60.8	8.7	4116	7	ACA26049
28	60.4	8.6	5355	7	AAD55819
29	60.4	8.6	60196	7	AAD55810
30	60.2	8.6	27541	4	AAD17185
31	60.2	8.6	125401	4	AAD17186
32	59.6	8.5	3957	5	AA09686
33	59.4	8.5	9975	7	AA161173
34	59.4	8.5	82746	7	AA161224
35	59.4	8.5	103599	4	ABX04971
36	59.4	8.5	103599	4	ABX04971
37	58.8	8.4	1167	7	AA161197
38	58.8	8.4	3810	7	ACA26366
39	58.8	8.4	13020	6	ABQ78873
40	58.8	8.4	113193	7	AAD54645
41	58.4	8.3	798	6	ABK88966
42	58.4	8.3	945	6	ABK88963
43	58.4	8.3	1289	6	AAZ24026
44	58.4	8.3	2205	5	AA586363
45	58.4	8.3	2903	6	ABZ11989

ALIGNMENTS

RESULT 1

ABL57895

ID ABL57895 standard; DNA; 702 BP.

XX ABL57895;

AC

XX

DT 11-SEP-2003 (revised)

DT 04-JUL-2002 (first entry)

XX

DE Partial hypersensitive reaction and pathogenicity, hrpB5 gene.

XX Hypersensitive reaction and pathogenicity; hrpB5; exo-polysaccharide;

KW xanthan gum; gene; ds.

XX	Xanthomonas campestris; pv vesicatoria.
OS	WO200078967-A1.
XX	28-DEC-2000.
PN	21-JUN-2000; 2000WO-FR001725.
XX	22-JUN-1999; 99FR-0007963.
PF	(RHOD.) RHODIA CHIM.
PD	Pierrard J, Simon J, Chevallereau P;
XX	WPI; 2001-102725/11.
XX	New Xanthomonas campestris bacteria strains for use in production of exo-
XX	polysaccharides are made non-virulent by inactivation of at least one
XX	virulence gene.
XX	Claim 19; Page 27; 33pp; French.
XX	The present invention relates to new Xanthomonas campestris bacteria
XX	strains made non-virulent by inactivation of at least one virulence gene
XX	but which have retained the capacity to produce exo-polysaccharides
XX	(preferably xanthan gum). One such virulence gene deleted to produce the
XX	bacterial strains was the hrpB5 gene (Hypersensitive Reaction and
XX	pathogenicity). The hrp genes are essential for pathogenicity in plants.
XX	The present sequence is a partial sequence of the hrpB5, used in an
XX	example from the invention. (Updated on 11-SEP-2003 to standardise OS
XX	field)
XX	Sequence 702 BP; 97 A; 233 C; 266 G; 106 T; 0 U; 0 Other;
SQ	Query Match 100.0%; Score 702; DB 5; Length 702;
	Best Local Similarity 100.0%; Pred. No. 9.1e-114; Indels 0; Gaps 0;
	Matches 702; Conservative 0; Mismatches 0;

QY	1	ATGCGTCTTTGGCTGAGGTCCACACCGGAGCGGTGGCGCTTGACTGCGAGGTGATCCCA	60
DB	1	ATGCGTCTTTGGCTGAGGTCCACACCGGAGCGGTGGCGCTTGACTGCGAGGTGATCCCA	60
QY	61	CGCAGGCGATTTGGCTGTGCTGGAATGTGACGAGCGGGTGCACAGGTGACGCGGCT	120
DB	61	CGCAGGCGATTTGGCTGTGCTGGAATGTGACGAGCGGGTGCACAGGTGACGCGGCT	120
QY	121	TGCGCGCAGCGCGCTGGCGGAGCGCCAGACGCGTGCAGAGCGCTGCTGACGCTGCCAA	180
DB	121	TGCGCGCAGCGCGCTGGCGGAGCGCCAGACGCGTGCAGAGCGCTGCTGACGCTGCCAA	180
QY	181	CGGCGAGGCGAGGCGCATTCCTTCAGGATGCCACGACAGGCGGCGAGCGGCTG	240
DB	181	CGGCGAGGCGAGGCGCATTCCTTCAGGATGCCACGACAGGCGGCGAGCGGCTG	240
QY	241	GGCTATGCCGCGCGGCTGGCGGCTGCGCGCTGACGCGGTGGAACGAGCGGCGGCGAT	300

Db 241 GCGTATGCCGCGGGCTGCGCGTCAAGCTCGAAGCGTGGACAGAGCGCGCGTGGCGCAT 300
Qy 301 GCGTTCGCGCGCCACGAGACGCGCGACCGCGCGCGCGCGCTGGCGCGAGATCGTCGCG 360
Db 301 GCGTTCGCGCGCCACGAGACGCGCGACCGCGCGCGCGCGCTGGCGCGAGATCGTCGCG 360
Qy 361 CAGCGCTGCGACGAGGTTCTGACAGGCGACGATCCTCGGCGCTGTACGCGCGCGCGCA 420
Db 361 CAGCGCTGCGACGAGGTTCTGACAGGCGACGATCCTCGGCGCTGTACGCGCGCGCGCA 420
Qy 421 CAGGCGCTGGAAGCGCGCGCTGAGAGAGCGAAAGCGCTGCGAGGTGAGCGTGCATCCGAT 480
Db 421 CAGGCGCTGGAAGCGCGCGCTGAGAGAGCGAAAGCGCTGCGAGGTGAGCGTGCATCCGAT 480
Qy 481 GCGCTGGAAGTGCAGCGCGCGCTTCGATCGCGCGCGCGCGCGCGCGCGATGAGCATG 540
Db 481 GCGCTGGAAGTGCAGCGCGCGCGCTTCGATCGCGCGCGCGCGCGCGCGCGATGAGCATG 540
Qy 541 CCGGTGGAAGTGTGCGGTGATACGACTCTGGCGCTTGGGTGCTGCTGCTGCTGCTGCTG 600
Db 541 CCGGTGGAAGTGTGCGGTGATACGACTCTGGCGCTTGGGTGCTGCTGCTGCTGCTGCTG 600
Qy 601 ACCGCGGTGTCGAGACCGATCTGCGTGTGATCAGCTGCGAGTCTCGCGCGCGTCAATCGC 660
Db 601 ACCGCGGTGTCGAGACCGATCTGCGTGTGATCAGCTGCGAGTCTCGCGCGCGTCAATCGC 660
Qy 661 CCGGTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 702
Db 661 CCGGTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 702

Search completed: July 7, 2004, 21:07:53
Job time : 209.168 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
OM nucleic - nucleic search, using sw model
Run on: July 7, 2004, 20:18:17 ; Search time 1351.57 Seconds
(without alignments)
18510.269 Million cell updates/sec

Title: US-10-018-786-7
Perfect score: 702
Sequence: 1 atgggtttttggtgaggtc.....cgggtgcggatggttctga 702
Scoring table: IDENTITY NJC
Gapop 10.0 , Gapext 1.0
Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pin:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rnd:*
26: em_gss_png:*
27: em_gss_vrl:*

28: gb_gss1:.*
 29: gb_gss2:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	83.4	11.9	935	29	CNS006XK
c 2	83.3	11.8	1131	29	AL066051 Drosophil
c 3	81.6	11.6	1244	12	AG042920 Pan trogl
4	77.4	11.0	1201	13	BGS46745 1024014H0
5	76.8	10.9	982	13	BX340009 BX340009
c 6	75.4	10.9	925	29	BX415111 BX415111
c 7	75.4	10.7	1452	29	AL053013 Drosophil
c 8	74.2	10.6	925	29	AG032979 Pan trogl
9	73	10.4	1023	29	AL053013 Drosophil
c 10	72.6	10.3	1134	29	AG128304 Pan trogl
c 11	72	10.3	893	28	AG043044 Pan trogl
c 12	71.8	10.2	1598	29	AZ193531 SP_1023 B
c 13	71.2	10.1	1101	29	AG030579 Pan trogl
c 14	71.2	10.1	1201	13	AG03543 Pan trogl
c 15	71	10.1	1104	29	BX340009 BX340009
16	70.8	10.1	932	29	AG062490 Pan trogl
c 17	70.8	10.1	1610	28	AL066742 Drosophil
c 18	70.6	10.1	1189	29	B2569386 pacs2-164
c 19	70.4	10.0	1421	28	AG030608 Pan trogl
c 20	70.2	10.0	1798	29	AG030608 Pan trogl
c 21	70	10.0	935	29	B2569488 pacs2-164
c 22	70	10.0	1438	28	AG171124 Pan trogl
c 23	70	10.0	1538	29	AL066051 Drosophil
c 24	69.4	9.9	1432	29	B2557931 pacs1-60
c 25	69.4	9.9	1626	10	AG030607 Pan trogl
c 26	69.2	9.9	896	29	AG032979 Pan trogl
c 27	69.2	9.9	1026	28	AW731212 GA_Ea001
c 28	69.2	9.9	1299	29	AG159205 Pan trogl
c 29	69.2	9.9	1348	29	B2569417 pacs2-164
c 30	68.8	9.8	1157	12	AG039481 Pan trogl
c 31	68.6	9.8	932	29	CG752544 P047-2-C1
c 32	68.6	9.8	1132	14	BM466479 AGENCOURT
c 33	68.4	9.7	1037	29	AL066742 Drosophil
c 34	68.4	9.7	1083	14	CK210297 FGASQ2209
c 35	68.2	9.7	1165	29	AL276477 Tetradon
c 36	68.2	9.7	1201	13	AG030649 Pan trogl
c 37	67.6	9.6	1387	10	BX405071 BX405071
c 38	67.4	9.6	1542	29	AW731151 GA_Ea001
c 39	67.2	9.6	1200	13	AG032943 Pan trogl
c 40	67	9.5	1120	29	BX415896 BX415896
c 41	66.6	9.5	842	29	AG136785 Pan trogl
c 42	66.4	9.5	1124	29	AG058791 Pan trogl
c 43	66.4	9.5	1232	29	AG041123 Pan trogl
c 44	66.4	9.5	1273	12	AG072425 Pan trogl
c 45	66.4	9.5	1277	29	BM562099 AGENCOURT
					AG060206 Pan trogl